

10615383.txt
 Title: US-10-615-383A-7_COPY_252_1895
 Perfect score: 1644
 Sequence: 1 gagaat acagt acaagacgt act tgcct cct gaaaaaact 1644

RESULT 3

ABN93014

ID ABN93014 standard; DNA; 2793 BP.

XX

AC ABN93014;

XX

DT 24-JUL-2002 (first entry)

XX

DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO: 2477.

XX

KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW antibacterial; gene therapy; gene; ds.

XX

CS Staphylococcus epidermidis.

XX

PN US6380370- B1.

XX

PD 30-APR-2002.

XX

PF 13-AUG-1998; 98US-00134001.

XX

PR 14-AUG-1997; 97US-0055779P.

XX

PR 08-NOV-1997; 97US-0064964P.

XX

PA (GENO) GENOME THERAPEUTICS CORP.

XX

PI Doucette-Stamm LA, Bush D;

XX

DR VPI; 2002-381255/41.

XX

DR P-PSDB; ABP40469.

XX

PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis

XX

PS polypeptide, useful for diagnosing and treating bacterial infections.

XX

XX Disclosure; SEQ ID NO 2477; 267pp; English.

CC

CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can
 CC also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life cycle
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site

XX

SQ Sequence 2793 BP; 1149 A; 423 C; 497 G; 724 T; 0 U; 0 Other;

Query Match 100.0% Score 1644; DB 1; Length 2793;

Best Local Similarity 100.0%

Matches 1644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGAATACAGTACAAGACGTTAAAGATTGGAATATGGATGATGAATTATCAGATAGCAAT 60
 Db 151 GAGAATACAGTACAAGACGTTAAAGATTGGAATATGGATGATGAATTATCAGATAGCAAT 210

Qy 61 GATCAGTCCAGTAATGAAGAAAAGATGATGTAATCAATAATAGTCAGTCAATAAACACC 120
 Db 211 GATCAGTCCAGTAATGAAGAAAAGATGATGTAATCAATAATAGTCAGTCAATAAACACC 270
 Qy 121 GATGATGATAAOCAAATAAAAAAGAAGAAAAGAAATAGCAACGATGCCATAGAAAATCGC 180
 Db 271 GATGATGATAAOCAAATAAAAAAGAAGAAAAGAAATAGCAACGATGCCATAGAAAATCGC 330
 Qy 181 TCTAAAGATATAACACAGTCAACAACAAATGTAGATGAAAAGAAAGCAACATTTTTACAA 240
 Db 331 TCTAAAGATATAACACAGTCAACAACAAATGTAGATGAAAAGAAAGCAACATTTTTACAA 390
 Qy 241 AAGACCCCTCAAGATAATACTCAGCTTAAAGAGAGAGTGGTAAAAGAACCCCTCATCAGTC 300
 Db 391 AAGACCCCTCAAGATAATACTCAGCTTAAAGAGAGAGTGGTAAAAGAACCCCTCATCAGTC 450
 Qy 301 GAATCCTCAAATTCATCAATGGATACTGCCAACAAACCATCTCATACAACAATAAATAGT 360
 Db 451 GAATCCTCAAATTCATCAATGGATACTGCCAACAAACCATCTCATACAACAATAAATAGT 510
 Qy 361 GAAGCATCTATTCAAAACAAGTGATAATGAAGAAAATTCCCGCGTATCAGATTTTGCTAAC 420
 Db 511 GAAGCATCTATTCAAAACAAGTGATAATGAAGAAAATTCCCGCGTATCAGATTTTGCTAAC 570
 Qy 421 TCTAAAAATATAGAGAGTAACACTGAATCCAATAAAGAGAGAAATACTATAGAGCAACCT 480
 Db 571 TCTAAAAATATAGAGAGTAACACTGAATCCAATAAAGAGAGAAATACTATAGAGCAACCT 630
 Qy 481 AACAAAGTAAGAGAAGATTCAATAACAAGTCAACCGTCTAGCTATAAAAAATATAGATGAA 540
 Db 631 AACAAAGTAAGAGAAGATTCAATAACAAGTCAACCGTCTAGCTATAAAAAATATAGATGAA 690
 Qy 541 AAAATTTCAAATCAAGATGAGTTATTAATTTACCAATAAATGAATATGAAAATTAAGGTT 600
 Db 691 AAAATTTCAAATCAAGATGAGTTATTAATTTACCAATAAATGAATATGAAAATTAAGGTT 750
 Qy 601 AGAOCGGTATCTACAACATCTGCCAACCATCGAGTAAGCGTGAACCGTAAATCAATTA 660
 Db 751 AGAOCGGTATCTACAACATCTGCCAACCATCGAGTAAGCGTGAACCGTAAATCAATTA 810
 Qy 661 GCGGCAGAACAAAGGTTGGAATGTTAATCATTTAATTAAGGTAAGTACTGATCAAAGTATTACT 720
 Db 811 GCGGCAGAACAAAGGTTGGAATGTTAATCATTTAATTAAGGTAAGTACTGATCAAAGTATTACT 870
 Qy 721 GAAGGATATGATGATAGTGATGGTATTATTAAGGCACATGATGCTGAAAACCTTAATCTAT 780
 Db 871 GAAGGATATGATGATAGTGATGGTATTATTAAGGCACATGATGCTGAAAACCTTAATCTAT 930
 Qy 781 GATGTAACCTTTTGAAGTAGATGATAAAGTGAAATCTGGTGATACGATGACAGTGAAATATA 840
 Db 931 GATGTAACCTTTTGAAGTAGATGATAAAGTGAAATCTGGTGATACGATGACAGTGAAATATA 990
 Qy 841 GATAAGAATACAGITTCATCAGATTTAACCGATAGTTTTGCAATACCAAAAAATAAAGAT 900
 Db 991 GATAAGAATACAGITTCATCAGATTTAACCGATAGTTTTGCAATACCAAAAAATAAAGAT 1050
 Qy 901 AATTCTGGAGAAATCATCGCTACAGGTAAGTATGACACACACAAATAAACAAATTACCTAC 960
 Db 1051 AATTCTGGAGAAATCATCGCTACAGGTAAGTATGACACACACAAATAAACAAATTACCTAC 1110
 Qy 961 ACTTTTACAGATTATGTAGATAAATATGAAAATATTAAAGGCGCACTTTAAATTAACTCA 1020
 Db 1111 ACTTTTACAGATTATGTAGATAAATATGAAAATATTAAAGGCGCACTTTAAATTAACTCA 1170

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Qy      1021 TACATTGATAAATCAAAGGTTCCAAATAATAACACTAAGTTAGATGTAGAATATAAGACG 1080
Db      1171 TACATTGATAAATCAAAGGTTCCAAATAATAACACTAAGTTAGATGTAGAATATAAGACG 1230

Qy      1081 GGCCTTTTCATCAGTAAATAAAACAATTACGGTTGAATATCAAAAACCTAACGAAAATCGG 1140
Db      1231 GGCCTTTTCATCAGTAAATAAAACAATTACGGTTGAATATCAAAAACCTAACGAAAATCGG 1290

Qy      1141 ACTGCTAACCTTCAAAGTATGTTCAAAACATAGATACGAAAACCATACAGTTGAGCAA 1200
Db      1291 ACTGCTAACCTTCAAAGTATGTTCAAAACATAGATACGAAAACCATACAGTTGAGCAA 1350

Qy      1201 ACGATTATATTAAOCTCTTGTTATTGAGCCAAAGAAACAAATGTAAATATTTGAGGG 1260
Db      1351 ACGATTATATTAAOCTCTTGTTATTGAGCCAAAGAAACAAATGTAAATATTTGAGGG 1410

Qy      1261 AATGGGATGAAGGTTCAACAATTATCGAGATAGTACAATCATTAAAGTTTATAAGGTT 1320
Db      1411 AATGGGATGAAGGTTCAACAATTATCGAGATAGTACAATCATTAAAGTTTATAAGGTT 1470

Qy      1321 GGAGATAATCAAAATTTAOCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGAT 1380
Db      1471 GGAGATAATCAAAATTTAOCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGAT 1530

Qy      1381 GTCACAAATGATGATTATGCCAATTAGGAAATAATAATGACGTGAATATTAATTTTGGT 1440
Db      1531 GTCACAAATGATGATTATGCCAATTAGGAAATAATAATGACGTGAATATTAATTTTGGT 1590

Qy      1441 AATATAGATTCAOCATATATTATTAAAGTATTAGTAAATATGAOCTAATAAGGACGAT 1500
Db      1591 AATATAGATTCAOCATATATTATTAAAGTATTAGTAAATATGAOCTAATAAGGACGAT 1650

Qy      1501 TACAOCAGATACAGCAAACCTGTGACAATGCAAAOAGCTATAAATGAGTATACTGGTGAG 1560
Db      1651 TACAOCAGATACAGCAAACCTGTGACAATGCAAAOAGCTATAAATGAGTATACTGGTGAG 1710

Qy      1561 TTTAGAACAGCATOCTATGATAATACAATTGCTTTCTCTACAAGTTCAGGTCAAGGACAA 1620
Db      1711 TTTAGAACAGCATOCTATGATAATACAATTGCTTTCTCTACAAGTTCAGGTCAAGGACAA 1770

Qy      1621 GGTGACTTGCTOCTGAAAAAACT 1644
Db      1771 GGTGACTTGCTOCTGAAAAAACT 1794

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Title: US-10-615-383A-7
 Perfect score: 2976
 Sequence: 1 atattgcaaaaaagacttat.....ccaacaaatataaggtgttg 2976

RESULT 4

US-09-134-001C-2477

: Sequence 2477, Application US/09134001C

: Patent No. 6380370

: GENERAL INFORMATION:

: APPLICANT: Lynn Doucette-Stamm et al

: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

STAPHYLOCOCCUS

: TITLE OF INVENTION: EPIDERMIS FOR DIAGNOSTICS AND THERAPEUTICS

: FILE REFERENCE: GTC-007

: CURRENT APPLICATION NUMBER: US/09/134,001C

: CURRENT FILING DATE: 1998-08-13

: PRIOR APPLICATION NUMBER: US 60/064,964

PRI OR FILING DATE: 1997-11-08
 PRI OR APPLI CATION NUMBER: US 60/055,779
 PRI OR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 2477
 LENGTH: 2793
 TYPE: DNA
 ORGANISM: *Staphylococcus epidermidis*
 US-09-134-001C-2477

Query Match 93.8% Score 2791.4; DB 3; Length 2793;
 Best Local Similarity 99.9%
 Matches 2792; Conservative 0; M smatches 1; Indels 0; Gaps 0;

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Qy      102 TTAATAAAAAAAAAAATTTACTAACTAAAAAGAAACCTATAGCAAAATAATCCAATAAATAT 161
Db      1  TTAATAAAAAAAAAAATTTACTAACTAAAAAGAAACCTATAGCAAAATAATCCAATAAATAT 60

Qy      162 GCAATTAGAAAAATTCACAGTAGGTACAGCGTCTATTGTAATAGGTGCAGCATTATTGTTT 221
Db      61 GCAATTAGAAAAATTCACAGTAGGTACAGCGTCTATTGTAATAGGTGCAACATTATTGTTT 120

Qy      222 GGTTTAGGTGATAATGAGGCCAAAGCTGAGGAGAATACAGTACAAGACGTTAAAGATTGG 281
Db      121 GGTTTAGGTGATAATGAGGCCAAAGCTGAGGAGAATACAGTACAAGACGTTAAAGATTGG 180

Qy      282 AATATGGATGATGAATTATCAGATAGCAATGATCAGTCCAGTAATGAAGAAAAGAAATGAT 341
Db      181 AATATGGATGATGAATTATCAGATAGCAATGATCAGTCCAGTAATGAAGAAAAGAAATGAT 240

Qy      342 GTAATCAATAATAGTCAGTCAATAAACACCGATGATGATAACCAAATAAAAAAGAGAA 401
Db      241 GTAATCAATAATAGTCAGTCAATAAACACCGATGATGATAACCAAATAAAAAAGAGAA 300

Qy      402 ACGAATAGCAACGATGCCATAGAAAATGGCTCTAAAGATATAACACAGTCAACACAAAT 461
Db      301 ACGAATAGCAACGATGCCATAGAAAATGGCTCTAAAGATATAACACAGTCAACACAAAT 360

Qy      462 GTAGATGAAAACGAAAGCAACATTTTTACAAAAGACCGCTCAAGATAATACTCAGCTTAAA 521
Db      361 GTAGATGAAAACGAAAGCAACATTTTTACAAAAGACCGCTCAAGATAATACTCAGCTTAAA 420

Qy      522 GAAGAAGTGGTAAAAAGAACCGCTCATCAGTGGAAATGCTCAAATTCATCAATGGATACTGCC 581
Db      421 GAAGAAGTGGTAAAAAGAACCGCTCATCAGTGGAAATGCTCAAATTCATCAATGGATACTGCC 480

Qy      582 CAACAACCATCTCATACAACAATAAATAGTGAAGCATCTATTCAAACAAGTGATAATGAA 641
Db      481 CAACAACCATCTCATACAACAATAAATAGTGAAGCATCTATTCAAACAAGTGATAATGAA 540

Qy      642 GAAAAATCCCGGTATCAGATTTTGCTAACTCTAAAAATAAGAGAGTAACTGAAATCC 701
Db      541 GAAAAATCCCGGTATCAGATTTTGCTAACTCTAAAAATAAGAGAGTAACTGAAATCC 600

Qy      702 AATAAGAGAGAGATACTATAGAGCAACCTAACAAAGTAAGAGAGATTCAATAACAAGT 761
Db      601 AATAAGAGAGAGATACTATAGAGCAACCTAACAAAGTAAGAGAGATTCAATAACAAGT 660

Qy      762 CAACCGTCTAGCTATAAAAAATATAGATGAAAAATTTCAAATCAAGATGAGTTATTAAAT 821
Db      661 CAACCGTCTAGCTATAAAAAATATAGATGAAAAATTTCAAATCAAGATGAGTTATTAAAT 720

Qy      822 TTACCAATAAATGAATATGAAAAAAGGTAGACGGTATCTACAACATCTGCCAACCA 881
  
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Db      721  TTACCAATAAATGAATATGAAATAAAGGTTAGACGGTTATCTACAACATCTGCCAAOCCA 780
Qy      882  TCGAGTAAOOGTGTAAOOGTAAATCAATTAGOGGCGAGAACAAAGGTTGSAATGTTAATCAT 941
Db      781  TCGAGTAAOOGTGTAAOOGTAAATCAATTAGOGGCGAGAACAAAGGTTGSAATGTTAATCAT 840
Qy      942  TTAATTTAAAGTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGATGGTATTATT 1001
Db      841  TTAATTTAAAGTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGATGGTATTATT 900
Qy     1002  AAAGCACATGATGCTGAAAACCTTAATCTATGATGTAACTTTTGAAGTAGATGATAAGGTG 1061
Db     901  AAAGCACATGATGCTGAAAACCTTAATCTATGATGTAACTTTTGAAGTAGATGATAAGGTG 960
Qy     1062  AAATCTGGTGATACGATGACAGTGAATATAGATAAGAAACACAGTTCATCAGATTTAACC 1121
Db     961  AAATCTGGTGATACGATGACAGTGAATATAGATAAGAAACACAGTTCATCAGATTTAACC 1020
Qy     1122  GATAGITTTTGCATACCAAAAAATAAAAGATAATTCTCGAGAAATCATCGCTACAGGTAAT 1181
Db     1021  GATAGITTTTGCATACCAAAAAATAAAAGATAATTCTCGAGAAATCATCGCTACAGGTAAT 1080
Qy     1182  TATGACAAACAAAAATAAACAAATTACCTACACTTTTACAGATTATGTAGATAAATATGAA 1241
Db     1081  TATGACAAACAAAAATAAACAAATTACCTACACTTTTACAGATTATGTAGATAAATATGAA 1140
Qy     1242  AATATTTAAAGGGCAOCTTAAATTAACATCATACATTGATAAATCAAAGGTTGCAAAATAT 1301
Db     1141  AATATTTAAAGGGCAOCTTAAATTAACATCATACATTGATAAATCAAAGGTTGCAAAATAT 1200
Qy     1302  AACACTAAGITTAGATGTAGAATATAAGAOGGOOCTTTTCATCAGTAAATAAAAACAATTAC 1361
Db     1201  AACACTAAGITTAGATGTAGAATATAAGAOGGOOCTTTTCATCAGTAAATAAAAACAATTAC 1260
Qy     1362  GITTGAATATCAAAAAOCTAAOAGAAAATOGGACTGCTAAOCTTCAAAGTATGTTCAACAA 1421
Db     1261  GITTGAATATCAAAAAOCTAAOAGAAAATOGGACTGCTAAOCTTCAAAGTATGTTCAACAA 1320
Qy     1422  ATAGATACGAAAAOCCATACAGITTGAGCAAAOAGTTTATATTAAOOCCTCTTGTTATTCA 1481
Db     1321  ATAGATACGAAAAOCCATACAGITTGAGCAAAOAGTTTATATTAAOOCCTCTTGTTATTCA 1380
Qy     1482  GCCAAAGAAACAAATGTAATATTTTCAAGGAATGGOGATGAAGGTTCAACAATTTATCGAC 1541
Db     1381  GCCAAAGAAACAAATGTAATATTTTCAAGGAATGGOGATGAAGGTTCAACAATTTATCGAC 1440
Qy     1542  GATAGTACAATCATTAAAGTATTATAAGGTTGGAGATAATCAAAATTTAOCAGATAGTAAC 1601
Db     1441  GATAGTACAATCATTAAAGTATTATAAGGTTGGAGATAATCAAAATTTAOCAGATAGTAAC 1500
Qy     1602  AGAATTTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCAATTATGGA 1661
Db     1501  AGAATTTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCAATTATGGA 1560
Qy     1662  AATAAATGAOCTGAATATTAATTTTGGTAATATAGATTCAOCCATATATTATTTAAAGTT 1721
Db     1561  AATAAATGAOCTGAATATTAATTTTGGTAATATAGATTCAOCCATATATTATTTAAAGTT 1620
Qy     1722  ATTAGTAAATATGAOCCATAAAGGAOAGTTACAOGAOGATACAGCAAACTGTGACAATG 1781
Db     1621  ATTAGTAAATATGAOCCATAAAGGAOAGTTACAOGAOGATACAGCAAACTGTGACAATG 1680

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Qy 1782 CAAACGACTATAAATGAGTATACTGGTGAGTTTGAACAGCATCTCTATGATAATACAATT 1841

Db 1681 CAAACGACTATAAATGAGTATACTGGTGAGTTTGAACAGCATCTCTATGATAATACAATT 1740

Qy 1842 GCTTTCTCTACAAGTTCAGGTCAAGGACAAGGTGACTTGCCTCTGAAAAAAGTTATAAA 1901

Db 1741 GCTTTCTCTACAAGTTCAGGTCAAGGACAAGGTGACTTGCCTCTGAAAAAAGTTATAAA 1800

Qy 1902 ATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAATACAAATGATAAT 1961

Db 1801 ATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAATACAAATGATAAT 1860

Qy 1962 GAAAAACCGCTTAGTAAATGATTGGTAACCTTTGAAGTATCCTGATGGAACCTTCAAAATCA 2021

Db 1861 GAAAAACCGCTTAGTAAATGATTGGTAACCTTTGAAGTATCCTGATGGAACCTTCAAAATCA 1920

Qy 2022 GTCAGAACAGATGAAGAGGGGAAATATCAATTTGATGGGTTAAAAAACGGATTGACTTAT 2081

Db 1921 GTCAGAACAGATGAAGAGGGGAAATATCAATTTGATGGGTTAAAAAACGGATTGACTTAT 1980

Qy 2082 AAAATTACATTGAAAAACCGGAAGGATATAAGCGGAGCTTAAACATTACGGAACAAAT 2141

Db 1981 AAAATTACATTGAAAAACCGGAAGGATATAAGCGGAGCTTAAACATTACGGAACAAAT 2040

Qy 2142 OCTGCACTAGACTCAGAAGGCAATTCGTATGGTAACCTATTAAOGGACAAGAGATATG 2201

Db 2041 OCTGCACTAGACTCAGAAGGCAATTCGTATGGTAACCTATTAAOGGACAAGAGATATG 2100

Qy 2202 ACTATTGATAGCGATTTTATCAAACACCTAAATATAGCTTAGGGAACCTATGTATGGTAT 2261

Db 2101 ACTATTGATAGCGATTTTATCAAACACCTAAATATAGCTTAGGGAACCTATGTATGGTAT 2160

Qy 2262 GACACTAATAAGATGGTATTCAAGGTGATGATGAAAAAGGAATCTCTGGAGTAAAAAGTG 2321

Db 2161 GACACTAATAAGATGGTATTCAAGGTGATGATGAAAAAGGAATCTCTGGAGTAAAAAGTG 2220

Qy 2322 ACGTTAAAAAGATGAAAAACGAAATATCATTAGTACAACAACAACTGATGAAAAAGGAAAG 2381

Db 2221 ACGTTAAAAAGATGAAAAACGAAATATCATTAGTACAACAACAACTGATGAAAAAGGAAAG 2280

Qy 2382 TATCAATTTGATAATTTAAATAGTGGTAATTATATTGTTCACTTTTGATAAAACCTTCAGGT 2441

Db 2281 TATCAATTTGATAATTTAAATAGTGGTAATTATATTGTTCACTTTTGATAAAACCTTCAGGT 2340

Qy 2442 ATGACTCAAAACAACAACAGATTCTGGTGATGATGAOGAACAGGATGCTGATGGGGAAGAA 2501

Db 2341 ATGACTCAAAACAACAACAGATTCTGGTGATGATGAOGAACAGGATGCTGATGGGGAAGAA 2400

Qy 2502 GTCCATGTAAACAATTACTGATCATGATGACTTTAGTATAGATAAOGGATACTATGATGAC 2561

Db 2401 GTCCATGTAAACAATTACTGATCATGATGACTTTAGTATAGATAAOGGATACTATGATGAC 2460

Qy 2562 GACTCAGATTAGATAGTGATTGACTCAGATAGCGAAGGACTCAGACTCCGATAGGGAT 2621

Db 2461 GACTCAGATTAGATAGTGATTGACTCAGATAGCGAAGGACTCAGACTCCGATAGGGAT 2520

Qy 2622 TCGACTCAGACAGGACTCAGATTCCGATAGTGATTGATTGAGATCAGACAGTGACTCAGAC 2681

Db 2521 TCGACTCAGACAGGACTCAGATTCCGATAGTGATTGATTGAGATCAGACAGTGACTCAGAC 2580

Qy 2682 TCAGATAGTGATTGATTGAGATCAGACAGGATTTCGACTCAGACAGTGACTCAGGATTAGAC 2741

Db 2581 TCAGATAGTGATTGATTGAGATCAGACAGGATTTCGACTCAGACAGTGACTCAGGATTAGAC 2640

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Qy      2742 AATAGCTCAGATAAGAATACAAAAGATAAAATTACGGGATACAGGAGCTAATGAAGATCAT 2801
Db      2641 AATAGCTCAGATAAGAATACAAAAGATAAAATTACGGGATACAGGAGCTAATGAAGATCAT 2700
Qy      2802 GATTCTAAAGGCACATTACTTGGAGCTTTATTTGCAGGTTTAGGAGCGTATTATTAGGG 2861
Db      2701 GATTCTAAAGGCACATTACTTGGAGCTTTATTTGCAGGTTTAGGAGCGTATTATTAGGG 2760
Qy      2862 AAGCGTGGCAAAAATAGAAAAAATAAAAAATTAA 2894
Db      2761 AAGCGTGGCAAAAATAGAAAAAATAAAAAATTAA 2793

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Title:      US-10-615-383A-10
Perfect score: 4824
Sequence:    1 LKKNLLTKKKPI ANKSNKY.....FAGLGALLLGKRRKNRKNKN 930

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RESULT 3

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ABP40469
ID      ABP40469 standard; protein; 930 AA.
XX
AC      ABP40469;
XX
DT      24-JUL-2002 (first entry)
XX
DE      Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5314.
XX
KW      Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW      antibacterial; gene therapy.
XX
OS      Staphylococcus epidermidis.
XX
PN      US6380370-B1.
XX
PD      30-APR-2002.
XX
PF      13-AUG-1998; 98US-00134001.
XX
PR      14-AUG-1997; 97US-0055779P.
PR      08-NOV-1997; 97US-0064964P.
XX
PA      (GENO-) GENOME THERAPEUTICS CORP.
XX
PI      Doucette-Stamm LA, Bush D;
XX
DR      VPI; 2002-381255/41.
DR      N-PSDB; ABN93014.
XX
PT      Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT      polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS      Disclosure; SEQ ID NO 5314; 267pp; English.
XX
CC      ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC      frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC      given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC      antibacterial activity and can be used in gene therapy. The sequences can
CC      also be used in the diagnosis and treatment of bacterial infections.
CC      particularly S. epidermidis infections. The sequences can be used to
CC      screen for compounds able to interfere with the S. epidermidis life cycle
CC      or inhibit S. epidermidis infection. N.B. The sequence data for this
CC      patent did not form part of the printed specification, but was obtained

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CC in electronic format directly from the USPTO web site

XX

SQ Sequence 930 AA;

Query Match 99.9% Score 4820; DB 1; Length 930;
 Best Local Similarity 99.9%
 Matches 929; Conservative 0; M smatches 1; Indels 0; Gaps 0;

Qy 1 LKKNLLTKKKPI ANKSNKYAI RKFTVGTASI VI GAALLFGLGHNEAKAEENTVQDVKDS 60
 Db 1 LKKNLLTKKKPI ANKSNKYAI RKFTVGTASI VI GATLLFGLGHNEAKAEENTVQDVKDS 60

Qy 61 NMDELSDSNQSSNEEKNDVI NNSQSI NTDDNQI KKEETNSNDI ENRSKI TQSTTN 120
 Db 61 NMDELSDSNQSSNEEKNDVI NNSQSI NTDDNQI KKEETNSNDI ENRSKI TQSTTN 120

Qy 121 VDENEATFLQKTPQDNTQLKEEVKPESSVESSNSSMOTACQPSHTTI NSEASI QTSUNE 180
 Db 121 VDENEATFLQKTPQDNTQLKEEVKPESSVESSNSSMOTACQPSHTTI NSEASI QTSUNE 180

Qy 181 ENSRVSDFANSKI I ESNTESNKEENTI EQPNKVPREDI TSQSPSYKNI DEKI SNQDELLN 240
 Db 181 ENSRVSDFANSKI I ESNTESNKEENTI EQPNKVPREDI TSQSPSYKNI DEKI SNQDELLN 240

Qy 241 LPI NEYENKVRPLSTTSACPSSKRVTVNQLAAEQGSNVNHLI KVTDCSI TEGYDSDGI I 300
 Db 241 LPI NEYENKVRPLSTTSACPSSKRVTVNQLAAEQGSNVNHLI KVTDCSI TEGYDSDGI I 300

Qy 301 KAHDAENLI YDVFVEVDDKVKSGDTMIVNI DKNTVPSDLTDSFAI PKI KDNSEI I ATGT 360
 Db 301 KAHDAENLI YDVFVEVDDKVKSGDTMIVNI DKNTVPSDLTDSFAI PKI KDNSEI I ATGT 360

Qy 361 YDNTNKQ TYTFTDYVDKYENI KAHLKLTSYI DSKVPNNNTKLDVEYKTALSSVNKTI T 420
 Db 361 YDNTNKQ TYTFTDYVDKYENI KAHLKLTSYI DSKVPNNNTKLDVEYKTALSSVNKTI T 420

Qy 421 VEYQKPENRNTALQSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVI SGNDEGSTI I D 480
 Db 421 VEYQKPENRNTALQSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVI SGNDEGSTI I D 480

Qy 481 DSTI I KVKYGVGNQLPDSNRI YDYSEYEDVTNDDYACLGNNDVNI NFGNI DSPYI I KV 540
 Db 481 DSTI I KVKYGVGNQLPDSNRI YDYSEYEDVTNDDYACLGNNDVNI NFGNI DSPYI I KV 540

Qy 541 I SKYDPNKDDYTTI QQTVTMQTTI NEYTGEFRITASYDNTI AFSTSSGCGGDLPEPKTYK 600
 Db 541 I SKYDPNKDDYTTI QQTVTMQTTI NEYTGEFRITASYDNTI AFSTSSGCGGDLPEPKTYK 600

Qy 601 I GDYWVEDVDKDI QNTNDNEKPLSNVLVLTLYPDGTSKSVRTDEEGKYQFDGLKNGLTY 660
 Db 601 I GDYWVEDVDKDI QNTNDNEKPLSNVLVLTLYPDGTSKSVRTDEEGKYQFDGLKNGLTY 660

Qy 661 KI TFTEPEGYPTLKHSGTNPALDSEGNVWWTI NGQDDMTI DSGFYQTPKYSLGNVWV 720
 Db 661 KI TFTEPEGYPTLKHSGTNPALDSEGNVWWTI NGQDDMTI DSGFYQTPKYSLGNVWV 720

Qy 721 DTNKDI QQDDEKI SGKVTLKDENGNI I STTTTDENGKYQFDNLNSGNYI VHFDPKSG 780
 Db 721 DTNKDI QQDDEKI SGKVTLKDENGNI I STTTTDENGKYQFDNLNSGNYI VHFDPKSG 780

Qy 781 MTQTITDSGDDDEQADGEEVHVTI TDHDDFSI DNGYDDSDSDSDSDSDSDSDSDSDSD 840
 Db 781 MTQTITDSGDDDEQADGEEVHVTI TDHDDFSI DNGYDDSDSDSDSDSDSDSDSDSDSD 840

Title: US-10-615-383A-10_OCPY_51_598
Perfect score: 2808
Sequence: 1 ENTVDVKDSNMDELSDSN.....TIAFSTSSCGCGDLPEKT 548

ABP40469

10 ABP40469 standard; protein; 930 AA.
 11 XX
 12 AC
 13 XX
 14 ABP40469;
 15 XX
 16 24- JUL- 2002 (first entry)
 17 XX
 18 Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO: 5314.
 19 XX
 20 Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 21 KW antibacterial; gene therapy.
 22 KW
 23 XX
 24 Staphylococcus epidermidis.
 25 OS
 26 XX
 27 US6380370- B1.
 28 PN
 29 XX
 30 30- APR- 2002.
 31 PD
 32 XX
 33 13- AUG- 1998; 98US- 00134001.
 34 PF
 35 XX
 36 14- AUG- 1997; 97US- 0055779P.
 37 PR
 38 08- NOV- 1997; 97US- 0064964P.
 39 PR
 40 XX
 41 (GENO) GENOME THERAPEUTICS CORP.
 42 PA
 43 XX
 44 Doucette- Stamm LA, Bush D;
 45 PI
 46 XX
 47 WPI; 2002- 381255/ 41.
 48 DR
 49 N- PSDB; ABN93014.
 50 DR
 51 XX
 52 Novel isolated nucleic acid encoding a Staphylococcus epidermis
 53 PT polypeptide, useful for diagnosing and treating bacterial infections.
 54 PT
 55 XX
 56 Disclosure; SEQ ID NO 5314; 267pp; English.
 57 PS
 58 XX
 59 ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 60 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 61 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
 62 CC antibacterial activity and can be used in gene therapy. The sequences can
 63 CC also be used in the diagnosis and treatment of bacterial infections,
 64 CC particularly S. epidermidis infections. The sequences can be used to
 65 CC screen for compounds able to interfere with the S. epidermidis life cycle
 66 CC or inhibit S. epidermidis infection. N.B. The sequence data for this
 67 CC patent did not form part of the printed specification, but was obtained
 68 CC in electronic format directly from the USPTO web site
 69 XX

SQ Sequence 930 AA;

Query Match 100.0% Score 2808; DB 1; Length 930;
 Best Local Similarity 100.0%
 Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  ENTVDQVKDSNMDELSDSNDQSSNEEKNDVI NNSQSI NTDDDNQI KKEETNSNDAI ENR 60
Db      51 ENTVDQVKDSNMDELSDSNDQSSNEEKNDVI NNSQSI NTDDDNQI KKEETNSNDAI ENR 110

Qy      61 SKDI TGSTTNVDENEATFLQKTPQDNTQLKEEWKEPSSVESSNSSMDTAQQPSHTTI NS 120
Db     111 SKDI TGSTTNVDENEATFLQKTPQDNTQLKEEWKEPSSVESSNSSMDTAQQPSHTTI NS 170

Qy     121 EASI QTSDNEENSRVSDFANSKI | ESNTESNKEENTI EQPNKVREDSI TSCQSSYKNI DE 180
Db     171 EASI QTSDNEENSRVSDFANSKI | ESNTESNKEENTI EQPNKVREDSI TSCQSSYKNI DE 230

Qy     181 KI SNQDELLNLPI NEYENKVRPLSTTSAQSSKRVTVNQLAAEGGSNNVHILI KVTQDSI T 240
Db     231 KI SNQDELLNLPI NEYENKVRPLSTTSAQSSKRVTVNQLAAEGGSNNVHILI KVTQDSI T 290

Qy     241 EGYDDSDGI | KAHDAAENLI YDVTFEVDDKVKSGDTMTVNI DKNTVPSDLTDSFAI PKI KD 300
Db     291 EGYDDSDGI | KAHDAAENLI YDVTFEVDDKVKSGDTMTVNI DKNTVPSDLTDSFAI PKI KD 350

Qy     301 NSGEI | ATGTYDNTNKQI TYTFTDYVDKYENI KAHLKLTSYI DKSQVPNNNTKLDVEYKT 360
Db     351 NSGEI | ATGTYDNTNKQI TYTFTDYVDKYENI KAHLKLTSYI DKSQVPNNNTKLDVEYKT 410

Qy     361 ALSSVNKTI TVEYQKPENRRTANLQSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVNI SG 420
Db     411 ALSSVNKTI TVEYQKPENRRTANLQSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVNI SG 470

Qy     421 NGDEGSTI | DDSTI | KVKYKGDNQNL PDSNRI YDYSEYEDVTNDDYACLGNNDVNI NFG 480
Db     471 NGDEGSTI | DDSTI | KVKYKGDNQNL PDSNRI YDYSEYEDVTNDDYACLGNNDVNI NFG 530

Qy     481 NI DSPYI | KVI SKYDPNKDDYTTI QQTVTMQITI NEYTGFEFRTASYDNTI AFSTSSGQGG 540
Db     531 NI DSPYI | KVI SKYDPNKDDYTTI QQTVTMQITI NEYTGFEFRTASYDNTI AFSTSSGQGG 590

Qy     541 GDLPEKT 548
Db     591 GDLPEKT 598

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